



APPENDIX A

ClustalW (v1.4) multiple sequence alignment

3 Sequences Aligned Alignment Score = 989
Gaps Inserted = 3 Conserved Identities = 35

Pairwise Alignment Mode: Slow

Pairwise Alignment Parameters:

Open Gap Penalty = 5.0 Extend Gap Penalty = 0.1
Similarity Matrix: blosum

Multiple Alignment Parameters:

Open Gap Penalty = 5.0 Extend Gap Penalty = 0.0
Delay Divergent = 40% Gap Distance = 8
Similarity Matrix: blosum

Processing time: 0.4 seconds

```
hu_Secs-1  1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
mu_Secs-1  1 MRLALSGLLCMLLLCFCIFSSEGRRHAPAKSLKLRR---CCHLSPRSKLT 47
ra_Secs-1  1 MRLTLSGLFFMLFLCLCVLSSEGRKRPAPKFPKLRP---RCHLSPRSKPI 47
          **** * * * . * ** .. *.***...*** * ** *
```

```
hu_Secs-1  51 NLKGHHVRLCKPCKLEPEPRLWVVPALPQV 81
mu_Secs-1  48 TWKGNHTRPCRLCRNKLVPKSWVVPALPQI 78
ra_Secs-1  48 TWKGNHTRPCRPCR-KLESNSWVVPALPQI 77
          . **.* * *. *. *****.
```